fungal *Aspergillus* species selected from the group consisting of *Aspergillus ustus (SEQ ID NO: 3), Aspergillus terreus (SEQ ID NO 4), Aspergillus niger (SEQ ID NO: 5), Aspergillus nidulans (SEQ ID NO: 6) Aspergillus fumigatus (SEQ ID NO: 7),* and *Aspergillus flavus (SEQ ID NO: 8),* is present in a sample, said method comprising the following steps:

a) extracting nucleic acid material from fungi contained in a patient sample from a patient suspected of having an *Aspergillus* infection;

b) adding two oligonucleotide primers, one of said primers consisting of SEQ ID NO:1 and the other primer consisting of SEQ ID NO:2, said primers bracketing a hypervariable region on the rRNA present in the fungal species of said group;

D2 Cont'd

c) amplifying the sequence between said primers; and

d) using one or more detectably labeled probes directed to a portion of the hypervariable region bracketed by said primers, said probes being selected from the group consisting of at least 15-25 contiguous nucleotides of SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7 and SEQ ID NO: 8 which distinguish said species, each said labeled probe being specific for one of said fungal species from said group, to determine whether said fungal species identified by each said labeled probe is present in said sample.

3. (Amended) The method of claim 2 wherein said amplifying procedure is the polymerase chain reaction.

4. (Amended) The method of claim 2 in which said one or more probes hybridize to a nucleic acid sequence encoding the internal spacer regions of a pathogenic *Aspergillus* species gene sequence and is selected from the group consisting of (SEQ ID NO:3), (SEQ ID NO:4), (SEQ ID NO:5), (SEQ ID NO:6), (SEQ ID NO:7), and (SEQ ID NO:8)[, (SEQ ID

NO:9), (SEQ ID NO:10), (SEQ ID NO:11), (SEQ ID NO:12), (SEQ ID NO:13), (SEQ ID NO:14), (SEQ ID NO:15), (SEQ ID NO:16), (SEQ ID NO:17), (SEQ ID NO:18), (SEQ ID NO:19), (SEQ ID NO:20), (SEQ ID NO:21), (SEQ ID NO:22) and (SEQ ID NO:23), (SEQ ID NO: 24),(SEQ ID NO:25),(SEQ ID NO:26),(SEQ ID NO:27),(SEQ ID NO:28), (SEQ ID NO:29),(SEQ ID NO:30), and (SEQ ID NO:31), (SEQ ID NO:32), (SEQ ID NO:33)].

D2 cont'd

5. (Amended) The method of claim 2 wherein, in step (d), more than one probe is used, each said probe being connected to (a) a different signal moiety or (b) a moiety which allows separation of said probes.

Please cancel claim 19 and add the following new claims.

20. (New) A method for determining which *Aspergillus* species selected from the group consisting of *Aspergillus ustus (SEQ ID NO: 3), Aspergillus terreus (SEQ ID NO: 4), Aspergillus niger (SEQ ID NO: 5), Aspergillus nidulans (SEQ ID NO: 6) Aspergillus fumigatus, (SEQ ID NO: 7),* and *Aspergillus flavus* (SEQ ID NO: 8) is present in a biological sample, said method comprising comparing the sequences of fungal nucleic acid extracted from said biological sample with the nucleic acid sequences of SEQ ID NOS: 3-8 to determine which pathogenic Aspergillus species is present in said biological sample.

D3

21. (New) A method for determining which Aspergillus species is present in a biological sample, said species being selected from the group consisting of *Aspergillus ustus (SEQ ID NO: 3), Aspergillus terreus (SEQ ID NO: 4), Aspergillus niger (SEQ ID NO: 5), Aspergillus nidulans (SEQ ID NO: 6) Aspergillus fumigatus, (SEQ ID NO: 7),* and *Aspergillus flavus* (SEQ ID NO: 8), said method comprising the steps of:

a) extracting fungal nucleic acid from said

biological sample;

b) generating restriction mapping patterns of said fungal nucleic acid; and

c) comparing said restriction mapping patterns of said fungal nucleic acid to the restriction mapping patterns of the nucleic acid sequences of SEQ ID NOS: 3-8, wherein identical restriction mapping patterns are indicative of which *Aspergillus* species is present in said biological sample.

D3 cont'd

22. (New) A method for determining which *Aspergillus* species selected from the group consisting of *Aspergillus ustus (SEQ ID NO: 3), Aspergillus terreus (SEQ ID NO: 4), Aspergillus niger (SEQ ID NO: 5), Aspergillus nidulans (SEQ ID NO: 6) Aspergillus fumigatus, (SEQ ID NO: 7),* and *Aspergillus flavus* (SEQ ID NO: 8) is present in a biological sample, said method comprising the steps of:

a) obtaining permeabilized tissue sections containing fungal nucleic acid from a patient;

b) contacting said permeabilized tissue sections with fluorescent molecular probes specific for pathogenic Aspergillus species comprising the sequences of SEQ ID NOS: 3-8; and

c) analyzing said permeabilized tissue section for said fluorescent molecular probes, the detection of which is indicative of the presence of pathogenic Aspergillus species in said biological sample.

A marked-up copy of the amendments are provided in Appendix A.

REMARKS

The October 19, 2001 Official Action and references cited therein have been carefully reviewed. In light of the amendments presented herewith and the following remarks, favorable reconsideration and allowance of the application are